L Number	Hits	Search Text	DB	Time stamp
1	178	glycoside adj hydrolase	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/07/05 11:27
7	678	carbohydrate adj binding	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/07/05 11:27
13	1	(glycoside adj hydrolase) and (carbohydrate adj binding)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/07/05 11:28
19	0	((glycoside adj hydrolase) and (carbohydrate adj binding)) and thermo	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/07/05 11:28

L Number	Hits	Search Text	DB	Time stamp
1	20718	glycoside hydrolase	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/07/05 10:00
7	178	glycoside adj hydrolase	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/07/05 10:01
13	35	acidothermus adj cellulolyticus	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/07/05 10:01
19	0	(glycoside adj hydrolase) and (acidothermus adj cellulolyticus)	USPAT; US-PGPUB; EPO; JPO; DERWENT	2002/07/05 10:01

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NEWS 17	Apr 22	BIOSIS Gene Names now available in TOXCENTER
NEWS 18	Apr 22	Federal Research in Progress (FEDRIP) now available
NEWS 19	Jun 03	New e-mail delivery for search results now available
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  69 FILES SEARCHED...
L2          368 L1 AND CATALYTIC (W) DOMAIN

=> s l2 and review
  42 FILES SEARCHED...
  79 FILES SEARCHED...
L3           19 L2 AND REVIEW

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=> d l4 1-14 bib ab

L4 ANSWER 1 OF 14 USPATFULL
AN 2001:231163 USPATFULL
TI Process of expressing and isolating recombinant proteins and recombinant protein products from plants, plant derived tissues or cultured plant cells
IN Shani, Ziv, Rehovot, Israel
Shoseyov, Oded, Karme Yosef, Israel
PA CBD Technologies Ltd., Rehovot, Israel (non-U.S. corporation)
Yissum Research and Development Company of the Hebrew University of Jerusalem, Jerusalem, Israel (non-U.S. corporation)
PI US 6331416 B1 20011218
AI US 1999-329234 19990610 (9)
DT Utility
FS GRANTED
EXNAM Primary Examiner: Campbell, Bruce R.; Assistant Examiner: Woitach, Joseph T.
CLMN Number of Claims: 11
ECL Exemplary Claim: 1
DRWN 1 Drawing Figure(s); 1 Drawing Page(s)
LN.CNT 1884
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A process of expressing a recombinant protein in a plant and of isolating the recombinant protein from the plant, the process is effected by (a) providing a plant, a plant derived tissue or cultured plant cells expressing a fusion protein including the recombinant protein and a cellulose binding peptide being fused thereto, the fusion protein being compartmentalized within cells of the plant, plant derived tissue or cultured plant cells, so as to be sequestered from cell walls of the cells of the plant, plant derived tissue or cultured plant cells; (b) homogenizing the plant, plant derived tissue or cultured plant cells, so as to bring into contact the fusion protein with a cellulosic matter of the plant, plant derived tissue or cultured plant cells, to thereby effect affinity binding of the fusion protein via the cellulose binding peptide to the cellulosic matter, thereby obtaining a fusion protein cellulosic matter complex; and (c) isolating the fusion protein cellulosic matter complex.

L4 ANSWER 2 OF 14 USPATFULL
AN 2001:121303 USPATFULL
TI Method and compositions for treating cellulose containing fabrics using truncated cellulase enzyme compositions
IN Fowler, Timothy, San Carlos, CA, United States
Clarkson, Kathleen A., San Francisco, CA, United States
Ward, Michael, San Francisco, CA, United States
Collier, Katherine D., Redwood City, CA, United States
Larenas, Edmund, Moss Beach, CA, United States
PA Genencor International, Inc., Rochester, NY, United States (U.S. corporation)
PI US 6268196 B1 20010731
AI US 1995-382452 19950201 (8)
RLI Continuation-in-part of Ser. No. US 1993-169948, filed on 17 Dec 1993
DT Utility
FS GRANTED
EXNAM Primary Examiner: Patterson, Jr., Charles L.

LREP Marcus-Werner, LynnGenecor International, Inc.
CLMN Number of Claims: 48
ECL Exemplary Claim: 1
DRWN 31 Drawing Figure(s); 24 Drawing Page(s)
LN.CNT 2131
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Improved methods of treating cellulose containing fabrics with cellulase comprising contacting the cellulose fabrics with truncated cellulase enzyme. Treatment of cellulose containing fabrics with cellulase core domains of the invention are disclosed as offering specific advantages of reduced redeposition of dye and increased abrasion.

L4 ANSWER 3 OF 14 USPATFULL
AN 2001:18258 USPATFULL
TI Method of releasing solid matrix affinity adsorbed particulates
IN Siegel, Daniel L., Rehovot, Israel
Shoseyov, Oded, Karme Yosef, Israel
PA CBD Technologies, LTD, Rehovot, Israel (non-U.S. corporation)
Yissum R&D Company of the Hebrew University, Jerusalem, Israel (non-U.S. corporation)
PI US 6184011 B1 20010206
AI US 1999-273268 19990322 (9)
DT Utility
FS Granted
EXNAM Primary Examiner: Chin, Christopher L.; Assistant Examiner: Do, Pensee T.
CLMN Number of Claims: 43
ECL Exemplary Claim: 1
DRWN 3 Drawing Figure(s); 2 Drawing Page(s)
LN.CNT 1809
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A method of releasing particulates from a solid matrix is provided. The method is effected adding to the solid matrix a degrading enzyme capable of degrading the solid matrix, to thereby release the particulates from the solid matrix.

L4 ANSWER 4 OF 14 USPATFULL
AN 2001:7867 USPATFULL
TI Purification of a polypeptide compound having a polysaccharide binding domain by affinity phase separation
IN Haynes, Charles A., Vancouver, Canada
Tomme, Peter, Vancouver, Canada
Kilburn, Douglas G., Vancouver, Canada
PA University of British Columbia, Vancouver, Canada (non-U.S. corporation)
PI US 6174700 B1 20010116
AI US 1995-505860 19950724 (8)
RLI Continuation-in-part of Ser. No. US 1994-249037, filed on 24 May 1994 Continuation of Ser. No. US 1992-865095, filed on 8 Apr 1992, now patented, Pat. No. US 5340731 Continuation-in-part of Ser. No. US 1990-603987, filed on 25 Oct 1990, now patented, Pat. No. US 5202247 Division of Ser. No. US 1988-216794, filed on 8 Jul 1988, now patented, Pat. No. US 5137819
DT Utility
FS Granted
EXNAM Primary Examiner: Naff, David M.
LREP Rae-Venter, BarbaraRae-Venter Law Group P.C.
CLMN Number of Claims: 34
ECL Exemplary Claim: 1
DRWN 25 Drawing Figure(s); 18 Drawing Page(s)
LN.CNT 2018
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A compound having a polysaccharide binding domain such as contained by a

cellulose and essentially lacking in polysaccharidase activity is purified from other ingredients in a mixture using an affinity partition system. A mixture containing the compound is contacted with a system containing as a first phase an aqueous solution of oligosaccharide polymer such as cellulose and as a second phase a solution of a polymer such as a poly(ethylene glycol)-poly(propylene glycol) copolymer. The compound petitions into the first phase and binds to the oligosaccharide polymer, preferably with a K.sub.a of 10.sup.3 to 10.sup.7, to form a complex. The complex is collected, and the compound is dissociated from the oligosaccharide polymer. The compound may be formed of a non-peptide chemical moiety or a peptide moiety linked to a polypeptide having the polysaccharide binding domain. The compound may also be a fusion polypeptide containing the polysaccharide binding domain linked through a protease recognition sequence to a macromolecule such as an enzyme, a hormone or an antibody. The macromolecule can be removed by using a protease to cleave the recognition sequence. Another partition system contains the oligosaccharide polymer and a phase separation inducing agent such as a sulfate or citrate salt that induces separation to produce different phases.

L4 ANSWER 5 OF 14 CAPLUS COPYRIGHT 2002 ACS
AN 2001:718269 CAPLUS
DN 135:239423
TI Cellulases of animal origin
AU Watanabe, Hirofumi
CS Natl. Inst. Agrobiol. Sci., Tsukuba, 305-8634, Japan
SO Journal of Applied Glycoscience (2001), 48(4), 343-351
CODEN: JAGLFX; ISSN: 1344-7882
PB Japanese Society of Applied Glycoscience
DT Journal; General Review
LA Japanese
AB A **review** with 58 refs. Their is still no significant change in the general view on cellulose digestion in animals, which is considered to be accomplished by symbiotes in the alimentary tracts. This is in spite of many expts. during the 20th century which have suggested the presence of endogenous cellulases in animals. In 1998, the first two examples of animal endogenous cellulase genes were isolated from plant cyst-nematodes and a termite. Since then, it has been conclusively shown that members of **glycoside-hydrolase** family (GHF) 5 are present in nematodes, GHF 9 members are present in termites, cockroaches, and crayfish, and a GHF 45 member is found in beetles. The GHF 9 members from these animals form an independent clade from other GHF 9 members. Thus it is supposed that a GHF 9 cellulase gene originated in an ancestral species among arthropods and was carried to the present species during the course of phylogenetic development. Different from fungal and bacterial cellulases, all animal cellulases, other than some of nematode origins, are composed only of a **catalytic domain**, which alone, is not effective in digesting the native form of cellulose so it is supposed that the animals in question developed an unique cellulose digesting system using the help of masticating organs.

L4 ANSWER 6 OF 14 BIOTECHNO COPYRIGHT 2002 Elsevier Science B.V.DUPLICATE
AN 2001:32217799 BIOTECHNO
TI Relationship of sequence and structure to specificity in the .alpha.-amylase family of enzymes
AU MacGregor E.A.; Janecek S.; Svensson B.
CS B. Svensson, Department of Chemistry, Carlsberg Laboratory, Gamle Carlsberg Vej 10, DK-2500 Copenhagen Valby, Denmark.
E-mail: bis@crc.dk
SO Biochimica et Biophysica Acta - Protein Structure and Molecular Enzymology, (09 MAR 2001), 1546/1 (1-20), 138 reference(s)
CODEN: BBAEDZ ISSN: 0167-4838

PUI S0167483800003022
DT Journal; General Review
CY Netherlands
LA English
SL English
AB The hydrolases and transferases that constitute the .alpha.-amylase family are multidomain proteins, but each has a **catalytic domain** in the form of a (.beta./.alpha.).sub.8-barrel, with the active site being at the C-terminal end of the barrel .beta.-strands. Although the enzymes are believed to share the same catalytic acids and a common mechanism of action, they have been assigned to three separate families - 13, 70 and 77 - in the classification scheme for **glycoside hydrolases** and transferases that is based on amino acid sequence similarities. Each enzyme has one glutamic acid and two aspartic acid residues necessary for activity, while most enzymes of the family also contain two histidine residues critical for transition state stabilisation. These five residues occur in four short sequences conserved throughout the family, and within such sequences some key amino acid residues are related to enzyme specificity. A table is given showing motifs distinctive for each specificity as extracted from 316 sequences, which should aid in identifying the enzyme from primary structure information. Where appropriate, existing problems with identification of some enzymes of the family are pointed out. For enzymes of known three-dimensional structure, action is discussed in terms of molecular architecture. The sequence-specificity and structure-specificity relationships described may provide useful pointers for rational protein engineering. .COPYRGT. 2001 Elsevier Science B.V.

L4 ANSWER 7 OF 14 FSTA COPYRIGHT 2002 IFIS
AN 2001(06):B0876 FSTA
TI Relationship of sequence and structure to specificity in the .alpha.-amylase family of enzymes.
AU MacGregor, E. A.; Janecek, S.; Svensson, B.
CS Correspondence (Reprint) address, B. Svensson, Dep. of Chem., Carlsberg Laboratory, Gamle Carlsberg Vej 10, DK-2500 Copenhagen Valby, Denmark. Fax +45-3327-4708. E-mail bis(a)crc.dk
SO Biochimica et Biophysica Acta, (2001), 1546 (1) 1-20, 138 ref. ISSN: 0005-2736
DT General Review
LA English
AB The relationship between sequence and specificity of the .alpha.-amylase family of enzymes, and the key structural features that contribute to specificity are reviewed. Although each enzyme in this family has a **catalytic domain** in the form of a (.beta./.alpha.).sub.8-barrel, they have been assigned to 3 separate families of the **glycoside hydrolases** and transferases (13, 70 and 77) based on amino acid sequence similarity. Motifs which are distinctive for each type of specificity are presented and problems with identification of certain enzymes are highlighted. It is suggested that the sequence-specificity and structure-specificity relationships described may be useful for rational protein engineering studies.

L4 ANSWER 8 OF 14 USPATFULL
AN 2000:43955 USPATFULL
TI Two-phase partition affinity separation system and affinity separated cell-containing composition
IN Haynes, Charles A., British Columbia, Canada
Tomme, Peter, British Columbia, Canada
Kilburn, Douglas G., British Columbia, Canada
PA Univ. of British Columbia, Vancouver, Canada (non-U.S. corporation)
PI US 6048715 20000411
AI US 1996-685808 19960724 (8)

RLI Continuation-in-part of Ser. No. US 1995-505860, filed on 24 Jul 1995 which is a continuation-in-part of Ser. No. US 1994-249037, filed on 24 May 1994 which is a continuation of Ser. No. US 1992-865095, filed on 8 Apr 1992, now patented, Pat. No. US 5340731 which is a continuation-in-part of Ser. No. US 1990-603987, filed on 25 Oct 1990, now patented, Pat. No. US 5202247 which is a division of Ser. No. US 1988-216794, filed on 8 Jul 1988, now patented, Pat. No. US 5137819
DT Utility
FS Granted
EXNAM Primary Examiner: Naff, David M.
LREP Rae-Venter Law Group, P.C.
CLMN Number of Claims: 22
ECL Exemplary Claim: 1
DRWN 26 Drawing Figure(s); 18 Drawing Page(s)
LN.CNT 2512
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB A two-phase partition system is provided for affinity separation of a composition containing a polysaccharide binding peptide from a mixture such as a fermentation broth. The peptide may be from an enzyme and lacking in polysaccharidase activity such as the binding domain of cellulase that binds to cellulose. The system contains a phase-forming oligosaccharide polymer such as a cellulose derivative to which the peptide binds with a Ka of 10.sup.3 M to 10.sup.7 M, and a phase inducing agent such as a polyethylene glycol polymer, or a salt present at sufficiently high concentration to induce phase separation. If the oligosaccharide polymer is thermoseparating, phase separation can be induced by heating. Using the system involves contacting a composition containing the peptide such as a fusion protein with the system, partitioning the composition into a phase containing the oligosaccharide polymer by binding to the polymer and recovering the polymer containing the bound composition. The peptide or a fusion protein containing the peptide can be contacted with a cell having a carbohydrate residue to which the peptide binds to form a complex, and the complex is separated with the system to produce a bound cell composition. The peptide may be linked through a protease recognition sequence to a macromolecule such as an enzyme, a hormone or an antibody, and the macromolecule can be removed by using a protease to cleave the recognition sequence.

L4 ANSWER 9 OF 14 CAPLUS COPYRIGHT 2002 ACS
AN 2001:20160 CAPLUS
DN 134:189778
TI **Glycoside hydrolases** and glycosyltransferases. Families, modules, and implications for genomics
AU Henrissat, Bernard; Davies, Gideon J.
CS Architecture et Fonction des Macromolecules Biologiques, Centre National de la Recherche Scientifique, Unite Mixte de Recherche 6098, Marseille, 13402, Fr.
SO Plant Physiology (2000), 124(4), 1515-1519
CODEN: PLPHAY; ISSN: 0032-0889
PB American Society of Plant Physiologists
DT Journal; General Review
LA English
AB A **review**, with 29 refs., on the system for classification of the **catalytic domains** of **glycoside hydrolases** and glycosyltransferases into families based on amino acid similarities.
RE.CNT 29 THERE ARE 29 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 10 OF 14 BIOTECHNO COPYRIGHT 2002 Elsevier Science B.V.DUPLICATE
AN 2000:30216108 BIOTECHNO
TI Structural features of normal and mutant human lysosomal

glycoside hydrolases deduced from bioinformatics analysis

AU Durand P.; Fabrega S.; Henrissat B.; Mornon J.-P.; Lehn P.

CS P. Lehn, Hopital Robert Debre, INSERM U458, 48 Boulevard Serurier, 75019 Paris, France.
E-mail: plehn@infobiogen.fr

SO Human Molecular Genetics, (12 APR 2000), 9/6 (967-977), 69 reference(s)
CODEN: HMGEE5 ISSN: 0964-6906

DT Journal; General Review

CY United Kingdom

LA English

SL English

AB Lysosomal storage diseases are due to inherited deficiencies in various enzymes involved in basic metabolic processes. As with other genetic diseases, accurate structure data for these enzymatic proteins should help in better understanding the molecular effects of mutations identified in patients with the corresponding lysosomal diseases; however, no such three-dimensional (3D) structure data are available for many lysosomal enzymes. Thus, we herein intend to illustrate for an audience of molecular geneticists how structure information can nonetheless be obtained via a bioinformatics approach in the case of five human lysosomal **glycoside hydrolases**. Indeed, using the two-dimensional hydrophobic cluster analysis method to decipher the sequence information available in data banks for the large group of **glycoside hydrolases** (clan GH-A) to which these human lysosomal enzymes belong, we could deduce structure predictions for their **catalytic domains** and propose explanations for the molecular effects of mutations described in patients. In addition, in the case of human .beta.-glucuronidase for which experimental 3D data have been reported, we also show here that bioinformatics methods relying on the available 3D structure information can be used to obtain further insights into the effects of various mutations described in patients with Sly disease. In a broader perspective, our work stresses that, in the context of a rapid increase in protein sequence information through genome sequencing, bioinformatics approaches might be highly useful for generating structure-function predictions based on sequence-structure interrelationships.

L4 ANSWER 11 OF 14 CAPLUS COPYRIGHT 2002 ACS

AN 2002:41829 CAPLUS

DN 136:196629

TI Microbial adherence to the plant cell wall and enzymatic hydrolysis

AU Forsberg, C. W.; Forano, E.; Chesson, A.

CS Department of Microbiology, University of Guelph, Guelph, ON, Can.

SO Ruminant Physiology: Digestion, Metabolism, Growth and Reproduction, [International Symposium on Ruminant Physiology], 9th, Pretoria, South Africa, Oct., 1999 (2000), Meeting Date 1999, 79-97. Editor(s): Cronje, Pierre B. Publisher: CABI Publishing, Wallingford, UK.
CODEN: 69CEVC; ISBN: 0-85199-463-6

DT Conference; General Review

LA English

AB A **review** discusses the mol. basis of adhesion and the improvement of adhesion abilities of rumen microorganisms to the plant particles. To examine the role in adhesion of microorganisms, the cellulose-binding proteins (CBP) is isolated, and the dockerin domains on polysaccharidase sequences and scaffoldins to identify enzymic complexes similar to cellulosomes are searched. Further understanding on the structure of the cellulosome and related cellulase systems of ruminal organisms and comparative studies on the cellulose-binding domain (CBD) and **catalytic domain** of ruminal and other organisms may reveal new opportunities to improve the catalytic properties of the ruminal cellulases. Topics discussed include diversity and catalytic

properties of bacterial, fungal, and protozoan **glycoside hydrolases**; structure and action of CBP; regulation of hydrolase synthesis and activity; and strategies to overcome limitations to the microbial degrdn. of plant cell walls.

RE.CNT 84 THERE ARE 84 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 12 OF 14 USPATFULL
AN 1999:24527 USPATFULL
TI Compositions and methods for modulating cell proliferation using growth factor-polysaccharide binding fusion proteins
IN Kilburn, Douglas G., Vancouver, Canada
Humphries, Keith R., Vancouver, Canada
Doheny, James G., Vancouver, Canada
Jervis, Eric, Vancouver, Canada
Alimonti, Judie, Vancouver, Canada
PA University of British Columbia, Canada (non-U.S. corporation)
PI US 5874308 19990223
AI US 1996-585585 19960116 (8)
DT Utility
FS Granted
EXNAM Primary Examiner: Kemmerer, Elizabeth C.
LREP Rae-Venter, Barbara, Kung, Viola T.Rae-Venter Law Group, P.C.
CLMN Number of Claims: 27
ECL Exemplary Claim: 1
DRWN 31 Drawing Figure(s); 31 Drawing Page(s)
LN.CNT 2617
CAS INDEXING IS AVAILABLE FOR THIS PATENT.
AB Methods and compositions are provided for in vitro expansion of growth factor dependent cells. Expansion is effected through the use of growth factor conjugates that include a growth factor such as a steel factor and a polysaccharidase substrate binding region. The conjugates are immobilized by binding of the substrate binding region to a substrate of the polysaccharidase in a growth chamber for the cells.

L4 ANSWER 13 OF 14 CAPLUS COPYRIGHT 2002 ACS
AN 1996:740887 CAPLUS
DN 126:16089
TI .beta.-1,4-Glycanases of Cellulomonas fimi: families, mechanisms, and kinetics
AU Bray, M. R.; Creagh, A. L.; Damude, H. G.; Gilkes, N. R.; Haynes, C. A.; Jervis, E.; Kilburn, D. G.; MacLeod, A. M.; Meinke, A.; et al.
CS Dep. Microbiology, Univ. British Columbia, Vancouver, BC, V6T 1Z3, Can.
SO ACS Symposium Series (1996), 655(Enzymes for Pulp and Paper Processing), 64-84
CODEN: ACSMC8; ISSN: 0097-6156
PB American Chemical Society
DT Journal; General Review
LA English
AB A **review** with 71 refs. Four endoglucanases, two cellobiohydrolases and a mixed function exoglucanase-xylanase from Cellulomonas fimi are modular proteins comprising from two to six domains. All of them contain a **catalytic domain** (CD) and at least one cellulose-binding domain (CBD). The CDs come from five of the families of **glycoside hydrolases**, and the CBDs from three of the families of CBDs, although all but one of the enzymes has a CBD from family II. The two cellobiohydrolases attack cellulose mols. from opposite ends. The Cs and the CBDs function independently of each other when sepd. by proteolysis or genetic engineering. The enzymes interact with cellulose in two ways. The CDs have weak affinity for substrate, relative to the CBDs, and catalyze hydrolysis of glycosidic bonds with inversion or retention of anomeric configuration, depending on

the CD. The CBDs have much greater affinities for cellulose, with Ka values of the order of 0.5-1.0 .mu.M for the family II CBDs. The family II CBDs adsorb to both cryst. and amorphous cellulose; the family IV CBD from endoglucanase CenC adsorbs to amorphous but not to cryst. cellulose. CBDCex from the exoglucanase-xylanase Cex, is a .beta.-barrel in soln., with extensive .beta.-sheet structure; three tryptophans, which participate in binding to cellulose, are adjacent in space and exposed on the surface of the .beta.-barrel. Adsorption of CBDCex to cryst. cellulose is entropically driven. Although CBDCex appears to bind irreversibly, the binding is dynamic and the polypeptide is mobile on the cellulose surface.

L4 ANSWER 14 OF 14 CAPLUS COPYRIGHT 2002 ACS
AN 1996:228295 CAPLUS
DN 124:282641
TI Interactions of cellulases from Cellulomonas fimi with cellulose
AU Din, N.; Coutinho, J.B.; Gilkes, N.R.; Jervis, E.; Kilburn, D.G.; Miller, R.C.; Ong, E.; Tomme, P.; Warren, R.A.J.
CS Department of Microbiology and Immunology, University of British Columbia, Vancouver, BC, V6T 1Z3, Can.
SO Prog. Biotechnol. (1995), 10(Carbohydrate Bioengineering), 261-70
CODEN: PBITE3; ISSN: 0921-0423
DT Journal; General Review
LA English
AB A **review**, with 54 refs. The amino acid sequences of eight .beta.-1,4-glycanases from Cellulomonas fimi are known from the nucleotide sequences of the corresponding genes. The enzymes, four endoglucanases, two cellobiohydrolases, a xylanase and a mixed function exoglucanase-xylanase, are all modular proteins comprising from two to six modules or domains. All of them contain a **catalytic domain** (CD) and a cellulose-binding domain (CBD). The CDs come from six of the families of **glycoside hydrolases**; the CBDs from three of the families of CBDs, although all but one of the enzymes has a CBD from family II. The CDs and the CBDs function independently of each other when sepd. by proteolysis or genetic engineering. The enzymes interact with cellulose/xylan in two ways. The CDs have weak affinity for substrate, relative to the CBDs, and catalyze hydrolysis of glycosidic bonds with inversion or retention of anomeric configuration, depending on the CD. The CBDs have much greater affinities for cellulose, with Kds of the order of 0.5-1.0 .mu.M for the family II CBDs. The family II CBDs, with the exception of CBDXylD from xylanase D, adsorb to both cryst. and amorphous cellulose; CBDXylD adsorbs only to cryst. cellulose. The family IV CBD from endoglucanase CenC (CBDCenC) absorbs to amorphous but not to cryst. cellulose. Adsorption to cellulose is strongly dependent on arom. amino acid residues, esp. tryptophans, which are conserved in nearly all family II CBDs. CBDCex from the exoglucanase-xylanase Cex, is a .beta.-barrel in soln., with extensive .beta.-sheet structure; two of the conserved tryptophans which participate in binding to cellulose are adjacent in space and exposed to solvent. The isolated CBDCenA, from endoglucanase CenA, has a disruptive effect on cotton fibers in spite of lacking hydrolytic activity. CBDCenA interacts synergistically with CDCenA in the release reducing sugars from cotton fibers. The binding of the family II CBDs to cellulose is stable enough for them to be used as affinity tags for protein purifn. and for enzyme immobilization.

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NEWS 5	Feb 19	Access via Tymnet and SprintNet Eliminated Effective 3/31/02
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NEWS 7	Mar 22	TOXLIT no longer available
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NEWS 9	Mar 28	US Provisional Priorities searched with P in CA/CAplus and USPATFULL
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  79 FILES SEARCHED...
 108 FILES SEARCHED...
L2          837 CARBOHYDRATE (W) BINDING (W) DOMAIN

=> s l1 and l2
  66 FILES SEARCHED...
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L3           11 L1 AND L2

=> s carbohydrate (w) binding
  31 FILES SEARCHED...
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L4        12365 CARBOHYDRATE (W) BINDING

=> s l1 and l4
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AN 2002:500403 CAPLUS
TI Prebleaching of kraft pulp with full-length and truncated forms of a **thermostable** modular xylanase from Rhodothermus marinus
AU Pfabigan, Notburga; Karlsson, Eva Nordberg; Ditzelmueller, Guenther; Holst, Olle
CS Holzforschung Austria, Franz-Grill Strasse 7, Vienna, A-1031, Austria
SO Biotechnology Letters (2002), 24(14), 1191-1197 > F.D
CODEN: BILED3; ISSN: 0141-5492
PB Kluwer Academic Publishers
DT Journal
LA English
AB Full-length and truncated forms of a modular **thermostable** xylanase (EC 3.2.1.8., **glycoside hydrolase** family 10) were used in bleaching sequences of hardwood and softwood kraft pulps. Enzymic treatment led to brightness gains of all pulps but the result depended on the pulp source. The presence of the addnl. domains in the full-length enzyme (including **carbohydrate-binding** modules) did not improve the bleaching process. No significant change in viscosity was seen after enzyme treatments indicating an unaffected pulp fiber length.

L7 ANSWER 2 OF 3 JICST-EPlus COPYRIGHT 2002 JST
AN 1010458437 JICST-EPlus
TI Importance of the **Carbohydrate-Binding** Module of Clostridium stercorarium Xyn10B to Xylan Hydrolysis.
AU ALI M K; HAYASHI H; KARITA S; GOTO M; KIMURA T; SAKKA K; OHMIYA K
CS Mie Univ., Tsu, Jpn
SO Biosci Biotechnol Biochem, (2001) vol. 65, no. 1, pp. 41-47. Journal Code: G0021A (Fig. 4, Tbl. 2, Ref. 41)
CODEN: BBBIEJ; ISSN: 0916-8451
CY Japan
DT Journal; Article
LA English
STA New
AB The Clostridium stercorarium xylanase Xyn10B is a modular enzyme comprising two **thermostabilizing** domains, a family 10 catalytic domain of glycosyl hydrolases, a family 9 **carbohydrate-binding** module(CBM), and two S-layer homologous(SLH) domains Biosci. Biotechnol. Biochem., 63, 1596-1604(1999)!. To investigate the role of this CBM, we constructed two derivatives of Xyn10B and compared their hydrolytic activity toward xylan and some preparations of plant cell walls; Xyn10B.DELTA.CBM consists of a catalytic domain only, and Xyn10B-CBM comprises a catalytic domain and a CBM. Xyn10B-CBM bound to various insoluble polysaccharides including Avicel, acid-swollen cellulose, ball-milled chitin, Sephadex G-25, and amyloseresin. A cellulose binding assay in the presence of soluble saccharides suggested that the CBM of Xyn10B had an affinity for even monosaccharides such as glucose, galactose, xylose, mannose and ribose. Removal of the CBM from the enzyme negated its cellulose- and xylan-binding abilities and severely reduced its enzyme activity toward insoluble xylan and plant cell walls but non soluble xylan. These findings clearly indicated that the CBM of Xyn10B is important in the hydrolysis of insoluble xylan. This is the first report of a family 9 CBM with an affinity for insoluble xylan in addition to crystalline cellulose and the ability to increase hydrolytic activity toward insoluble xylan. (author abst.)

L7 ANSWER 3 OF 3 JICST-EPlus COPYRIGHT 2002 JST
AN 1010288112 JICST-EPlus
TI Cloning, Sequencing, and Expression of the Gene Encoding a Cell-bound Multi-domain Xylanase from Clostridium josui, and Characterization of the Translated Product.
AU FENG J-X; KARITA S; FUJINO E; KIMURA T; SAKKA K; OHMIYA K

FUJINO T
CS Mie Univ., Tsu, Jpn
Nagoya Seiraku Co. Ltd., Nagoya, Jpn
SO Biosci Biotechnol Biochem, (2000) vol. 64, no. 12, pp. 2614-2624. Journal Code: G0021A (Fig. 10, Ref. 50)
CODEN: BBBIEJ; ISSN: 0916-8451
CY Japan
DT Journal; Article
LA English
STA New
AB The nucleotide sequence of the Clostridium josui FERM P-9684 xyn10A gene, encoding a xylanase Xyn10A, consists of 3,150bp and encodes 1,050 amino acids with a molecular weight of 115,564. Xyn10A is a multidomain enzyme composed of an N-terminal signal peptide and six domains in the following order: two **thermostabilizing** domains, a family 10 xylanase domain, a family 9 **carbohydrate-binding** module(CBM), and two S-layer homologous(SLH) domains. Immunological analysis indicated the presence of Xyn10A in the culture supernatant of C. josui FERM P-9684 and on the cell surface. The full-length Xyn10A expressed in a recombinant Escherichia coli strain bound to ball-milled cellulose(BMC) and the cell wall fragments of C. josui, indicating that both the CBM and the SLH domains are fully functional in the recombinant enzyme. An 85-kDa xylanase species derived from Xyn10A by partial proteolysis at the C-terminal side, most likely at the internal region of the CBM, retained the ability to bind to BMC. This observation suggests that the catalytic domain or the **thermostabilizing** domains are responsible for binding of the enzyme to BMC. Xyn10A-II, the 100-kDa derivative of Xyn10A, was purified from the recombinant E. coli strain and characterized. The enzyme was highly active toward xylan but not toward p-nitrophenyl-.BETA.-D-xylopyranoside, p-nitrophenyl-.BETA.-D-cellobioside, or carboxymethylcellulose. (author abst.)

Ding
Adney
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2/28/2001